

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL  
PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0213 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 219 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Val	Lys	Tyr	Phe	Leu	Gly	Gln	Ser	Val	Leu	Arg	Ser	Ser	Trp	Asp
1				5				10						15	
Gln	Val	Phe	Ala	Ala	Phe	Trp	Gln	Arg	Tyr	Pro	Asn	Pro	Tyr	Ser	Lys
			20				25						30		

PF-0213 US

His	Val	Leu	Thr	Glu	Asp	Ile	Val	His	Arg	Glu	Val	Thr	Pro	Asp	Gln
	35						40				45				
Lys	Leu	Leu	Ser	Arg	Arg	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Met	Pro	Arg
	50					55				60					
Trp	Ala	Glu	Arg	Leu	Phe	Pro	Ala	Asn	Val	Ala	His	Ser	Val	Tyr	Val
65				70					75					80	
Leu	Glu	Asp	Ser	Ile	Val	Asp	Pro	Gln	Asn	Gln	Thr	Met	Thr	Thr	Phe
			85					90					95		
Thr	Trp	Asn	Ile	Asn	His	Ala	Arg	Leu	Met	Val	Val	Glu	Glu	Arg	Cys
		100					105				110				
Val	Tyr	Cys	Val	Asn	Ser	Asp	Asn	Ser	Gly	Trp	Thr	Glu	Ile	Arg	Arg
	115					120				125					
Glu	Ala	Trp	Val	Ser	Ser	Ser	Leu	Phe	Gly	Val	Ser	Arg	Ala	Val	Gln
	130					135				140					
Glu	Phe	Gly	Leu	Ala	Arg	Phe	Lys	Ser	Asn	Val	Thr	Lys	Thr	Met	Lys
145				150					155					160	
Gly	Phe	Glu	Tyr	Ile	Leu	Ala	Lys	Leu	Gln	Gly	Glu	Ala	Pro	Ser	Lys
			165					170					175		
Thr	Leu	Val	Glu	Thr	Ala	Lys	Glu	Ala	Lys	Glu	Lys	Ala	Lys	Glu	Thr
		180					185					190			
Ala	Leu	Ala	Ala	Thr	Glu	Lys	Ala	Lys	Asp	Leu	Ala	Ser	Lys	Ala	Ala
	195					200					205				
Thr	Lys	Lys	Gln	Gln	Gln	Gln	Gln	Gln	Phe	Val					
	210					215									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGTGGTGA	CTGAGCTACG	AGCCTGGCGG	CGGGTGTGCG	CCGAGCCCCG	GCCCCGCCCCG	60
GCCCTCGCGT	GCCTCCCAGG	CTCCGCACCC	CTGATGCTGC	GCGGGTGCTG	AGCCCGCTTC	120
GGCCGGGACG	ATGGTGAAGT	ATTTCTGGG	CCAGAGCGTG	CTCCGGAGTT	CCTGGGACCA	180
AGTGTTGCGC	GCCTTCTGGC	AGCGGTACCC	GAATCCCTAT	AGCAAACATG	TCTTGACGGA	240
AGACATAGTA	CACCGGGAGG	TGACCCCTGA	CCAGAAACTG	CTGTCCCGGC	GACTCCTGAC	300
CAAGACCAAC	AGGATGCCAC	GCTGGGCCGA	GCGACTATTT	CCTGCCAATG	TTGCTCACTC	360
GGTGTACGTC	CTGGAGGACT	CTATTGTGGA	CCCACAGAAT	CAGACCATGA	CTACCTTCAC	420
CTGGAACATC	AACCACGCC	GGCTGATGGT	GGTGGAGGAA	CGATGTGTTT	ACTGTGTGAA	480
CTCTGACAAC	AGTGGCTGGA	CTGAAATCCG	CCGGGAAGCC	TGGGTCTCCT	CTAGCTTATT	540
TGGTGTCTCC	AGAGCTGTCC	AGGAATTTGG	TCTTGCCCGG	TTCAAAAGCA	ACGTGACCAA	600
GACTATGAAG	GGTTTTGAAT	ATATCTTGGC	TAAGCTGCAA	GGCGAGGCC	CTTCCAAAAC	660
ACTTGTTGAG	ACAGCCAAGG	AAGCCAAGGA	GAAGGCAAAG	GAGACGGCAC	TGGCAGCTAC	720
AGAGAAGGCC	AAGGACCTCG	CCAGCAAGGC	GGCCACCAAG	AAGCAGCAGC	AGCAGCAACA	780
GTTTGTGTAG	CCAGTCTACC	ACCACCACAG	CACCCACAGC	AGCTAGGCTT	AGCCCCTCTG	840
CCCTCCCTTC	ATTGTACT					858

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 969170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met 1	Gly	Lys	Tyr	Cys 5	Ala	Ser	Leu	Gly	Val 10	Leu	Lys	Gly	Pro	Trp 15	Asp
Gln	Val	Phe	Ala	Ala	Phe	Trp	Gln	Arg	Tyr 25	Pro	Asn	Pro	Tyr	Ser	Lys
His	Val	Leu	Thr	Glu	Asp	Ile	Val 40	His	Arg	Glu	Val	Thr 45	Ala	Asp	His
Lys	Leu	Leu	Ser	Arg	Arg	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Met	Pro	Arg
Trp 65	Ala	Glu	Arg	Phe	Phe	Pro	Ala	Asn	Val	Ala	His	Asn	Val	Tyr	Ile
Val	Glu	Asp	Ser	Ile	Val	Asp	Pro	Lys	Asn	Arg	Thr	Met	Thr	Thr	Phe
Thr	Trp	Asn	Ile	Asn	His	Ala	Arg	Leu	Met	Ala	Val	Glu	Glu	Arg	Cys
Val	Tyr	Arg	Val	Asn	Pro	Glu	Asn	Ser	Ser	Trp	Thr	Glu	Val	Lys	Arg
Glu	Ala	Trp	Val	Ser	Ser	Ser	Leu	Phe	Gly	Val	Ser	Arg	Ala	Val	Gln
Glu 145	Phe	Gly	Leu	Ala	Arg	Phe	Lys	Ser	Asn	Val	Thr	Lys	Ser	Thr	Lys
Gly	Phe	Glu	Tyr	Val	Leu	Ala	Arg	Met	Gln	Gly	Glu	Ala	Pro	Ser	Lys
Thr	Leu	Val	Glu	Thr	Ala	Lys	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Glu	Thr
Ala	Leu	Ala	Ala	Thr	Glu	Lys	Ala	Lys	Asp	Leu	Ala	Ser	Lys	Ala	Ala
Thr	Lys	Lys	Lys	Gln	Phe	Val									